

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: DAUGHERTY, BRUCE L.  
DEMARTINO, JULIE A.  
SICILIANO, SALVATORE J.  
SPRINGER, MARTIN S.
- (ii) TITLE OF THE INVENTION: EOSINOPHIL EOTAXIN RECEPTOR
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Merck & Co., Inc.  
(B) STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
(C) CITY: Rahway  
(D) STATE: NJ  
(E) COUNTRY: USA  
(F) ZIP: 07065-0900
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 60/016,158  
(B) FILING DATE: 26-APR-1996
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Eric Thies, J.  
(B) REGISTRATION NUMBER: 35,382  
(C) REFERENCE/DOCKET NUMBER: 19634Y
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 908-594-3904  
(B) TELEFAX: 908-594-4720  
(C) TELEX:

00922895 080601  
109080 56822660

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Thr	Thr	Ser	Leu	Asp	Thr	Val	Glu	Thr	Phe	Gly	Thr	Thr	Ser	Tyr
1				5					10					15	
Tyr	Asp	Asp	Val	Gly	Leu	Leu	Cys	Glu	Lys	Ala	Asp	Thr	Arg	Ala	Leu
			20					25					30		
Met	Ala	Gln	Phe	Val	Pro	Pro	Leu	Tyr	Ser	Leu	Val	Phe	Thr	Val	Gly
		35					40					45			
Leu	Leu	Gly	Asn	Val	Val	Val	Val	Met	Ile	Leu	Ile	Lys	Tyr	Arg	Arg
	50					55					60				
Leu	Arg	Ile	Met	Thr	Asn	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp
65					70					75				80	
Leu	Leu	Phe	Leu	Val	Thr	Leu	Pro	Phe	Trp	Ile	His	Tyr	Val	Arg	Gly
			85						90					95	
His	Asn	Trp	Val	Phe	Gly	His	Gly	Met	Cys	Lys	Leu	Leu	Ser	Gly	Phe
			100					105					110		
Tyr	His	Thr	Gly	Leu	Tyr	Ser	Glu	Ile	Phe	Phe	Ile	Ile	Leu	Leu	Thr
		115					120					125			
Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Ala	Val	Phe	Ala	Leu	Arg	Ala
	130					135						140			
Arg	Thr	Val	Thr	Phe	Gly	Val	Ile	Thr	Ser	Ile	Val	Thr	Trp	Gly	Leu
145					150					155					160
Ala	Val	Leu	Ala	Ala	Leu	Pro	Glu	Phe	Ile	Phe	Tyr	Glu	Thr	Glu	Glu
			165						170					175	
Leu	Phe	Glu	Glu	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Pro	Glu	Asp	Thr	Val
		180						185					190		
Tyr	Ser	Trp	Arg	His	Phe	His	Thr	Leu	Arg	Met	Thr	Ile	Phe	Cys	Leu
		195					200					205			
Val	Leu	Pro	Leu	Leu	Val	Met	Ala	Ile	Cys	Tyr	Thr	Gly	Ile	Ile	Lys
	210					215						220			
Thr	Leu	Leu	Arg	Cys	Pro	Ser	Lys	Lys	Lys	Tyr	Lys	Ala	Ile	Arg	Leu
225					230					235					240
Ile	Phe	Val	Ile	Met	Ala	Val	Phe	Phe	Ile	Phe	Trp	Thr	Pro	Tyr	Asn
			245						250					255	
Val	Ala	Ile	Leu	Ser	Ser	Tyr	Gln	Ser	Ile	Leu	Phe	Gly	Asn	Asp	
		260					265					270			
Cys	Glu	Arg	Ser	Lys	His	Leu	Asp	Leu	Val	Met	Leu	Val	Thr	Glu	Val
		275					280					285			
Ile	Ala	Tyr	Ser	His	Cys	Cys	Met	Asn	Pro	Val	Ile	Tyr	Ala	Phe	Val
	290					295					300				
Gly	Glu	Arg	Phe	Arg	Lys	Tyr	Leu	Arg	His	Phe	Phe	His	Arg	His	Leu
305					310					315					320
Leu	Met	His	Leu	Gly	Arg	Tyr	Ile	Pro	Phe	Leu	Pro	Ser	Glu	Lys	Leu
			325						330					335	
Glu	Arg	Thr	Ser	Ser	Val	Ser	Pro	Ser	Thr	Ala	Glu	Pro	Glu	Leu	Ser
			340					345					350		

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Ile Val Phe  
355

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGACAACCT CACTAGATAC AGTTGAGACC TTTGGTACCA CATCCTACTA TGATGACGTG  
60  
GGCCTGCTCT GTGAAAAAGC TGATAACCAGA GCACTGATGG CCCAGTTTGT GCCCCCGCTG  
120  
TACTCCCTGG TGTTCACTGT GGGCCTCTTG GGCAATGTGG TGGTGGTGAT GATCCTCATA  
180  
AAATACAGGA GGCTCCGAAT TATGACCAAC ATCTACCTGC TCAACCTGGC CATTTTCGGAC  
240  
CTGCTCTTCC TCGTCACCCT TCCATTCTGG ATCCACTATG TCAGGGGGCA TAACTGGGTT  
300  
TTTGGCCATG GCATGTGTAA GCTCCTCTCA GGGTTTTATC ACACAGGCTT GTACAGCGAG  
360  
ATCTTTTTCA TAATCCTGCT GACAATCGAC AGGTACCTGG CCATTGTCCA TGCTGTGTTT  
420  
GCCCTTCGAG CCCGGACTGT CACTTTTGGT GTCATCACCA GCATCGTCAC CTGGGGCCTG  
480  
GCAGTGCTAG CAGCTCTTCC TGAATTTATC TTCTATGAGA CTGAAGAGTT GTTTGAAGAG  
540  
ACTCTTTGCA GTGCTCTTTA CCCAGAGGAT ACAGTATATA GCTGGAGGCA TTTCCACACT  
600  
CTGAGAATGA CCATCTTCTG TCTCGTTCTC CCTCTGCTCG TTATGGCCAT CTGCTACACA  
660  
GGAATCATCA AAACGCTGCT GAGGTGCCCC AGTAAAAAAA AGTACAAGGC CATCCGGCTC  
720  
ATTTTTGTCA TCATGGCGGT GTTTTTTCATT TTCTGGACAC CCTACAATGT GGCTATCCTT  
780  
CTCTCTTCCT ATCAATCCAT CTTATTTGGA AATGACTGTG AGCGGAGCAA GCATCTGGAC  
840  
CTGGTCATGC TGGTGACAGA GGTGATCGCC TACTCCCACT GCTGCATGAA CCCGGTGATC  
900  
TACGCCTTTG TTGGAGAGAG GTTCCGGAAG TACCTGCGCC ACTTCTTCCA CAGGCACTTG  
960  
CTCATGCACC TGGGCAGATA CATCCCATT CTTCTAGTG AGAAGCTGGA AAGAACCAGC  
1020  
TCTGTCTCTC CATCCACAGC AGAGCCGGA CTCTCTATTG TGTTT  
1065

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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GGATCCCTAC CTTCCCCATC AGAGCTAGGG GGCATGGAGC GCTCTCTGCT AAGATGGGGA
60
CCCCCAAGGA ATGTCTCCCT GTGGGGCACT TCCTTACCAG ATGGGATGGC CAGTGCGGTT
120
AAGTTGGTGG TCAGGCAGAA AAAAAAGATC TAGTTTGTAC TCTTGAGAGT TCCTCGGTTT
180
GTTTCATGGCA TGGGCAGGGA GTCAAGGAGC AGCAGCCTTG CCTCAGTGCC TACCAGTGCA
240
GGAAAAGGTG CATAGCCTGG GCCAGGGCCA GGGCCCTGGT GGAGGCGTAG TGGTAACAGA
300
GAGGGCTCTC CATTCCAGCC CAAGGAAGAC TAAGAATGAA TACCTCATGA GTATATTAGC
360
TACAAACCAC CACAGCAGGT TCCAGAAAAA GGCTCAGCGT TGGAACCAGG TCACCCCCAC
420
TCAGCAGACA CCAGTCATAT AAATCAAGGA CCAACAGGAG ACAGGAACAC CCCCTTCCCA
480
CTCTGCCCCA TGTCTCAAGT TGTAGTGGCC CTTCTCCAG ATCTCTGCCA CCATCTTAGA
540
AAGGAACACT GAAAGAAGAA ACTGAAATTA TAAGCTGACA GCATAAAGAG GATGAGTAAA
600
ACCTAAAATC ATTGTTTACA TGAATGAATC AAGAGAAGTT TAAACCACTT TGGACTAAAA
660
TGTGTGAATC CTTTTTCCTG CTATCCAGCA GATGAGAAGC TGGTAACAGA GACCACAATA
720
GTTTGGAGAC TAAAGAATCA TTGCACATTT CACTGCTGAG TTGTATTGTG AGTAATTTTA
780
GTTGACCTCA CTTTGTAAAT CTTCACACG GGGCAATCCA ATATCTGCAC AAGAGATATG
840
TTAACCAGTG GTAAATGCTG CATGAGGAGA TTGGGTGATT TTTACTTTTCG TTTTGTGCT
900
CTTCTTTCTT ATTGTTCTTA CTTATTTACG ATTACCCTAT CGTTTTCCCA AAATGTAAAA
960
GGCCATTTTG AAAGCCTAAT TCAAACCTCT TCACTATTTT GTATCTAAGT ATTCACCTTG
1020
ATTGAGACTG GGTAGACAGG TGAAAACCAT ATCAGGTTTT TAATTTTTTA ATTTTAAATT
1080
ATTTATTTAT TTATTTATTT TTTGAGATGG AGTCTGGCTG TCGCCCAGGC TGGAGTGCAG
1140
CGGCGTGATC ACAGTTCAC TGCAGCTCAA CCTTCTAGGC TCAAGGGATT CTCCCACCTC
1200
AGCCCCCAA GTAGTTGGGA CCACACGTAT GCGCCACCAT GCCTGGCTAA TTTCTTATTT
1260
TTTTGTAGAG ATAGGATCTC ACTATATTGT CCAGGCTGGT CTTGAATTCC TGGGCTCAGG
1320

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TTAGAGGATT TTGAACAAAT TACTAAATTT CTTCAAGGTT CAATTTCCCC ATTAACATA  
3060  
ATGAATGTCT CATCATTATG GGGCCCTGGA GAAGCATAAT TACTTGTAAT TGTAATAATC  
3120  
ATTGTTATTA TTATTATACA TATTTTGCTT TTAAATGGAT AAGGATTTTT AAGGTATATG  
3180  
TAAACTGTAA AACATAAAAT GCAAAATGCC GTAAGAGACA GTAGTAATAA TAATGATTAT  
3240  
TATATTGTTA TCATTATCTA GCCTGTTTTT TCCTGTTGTG TATTTCTTCC TTAAATGCT  
3300  
TACAGAAATC TGTATCCCCA TTCTTCACCA CCACCCACAC ACATTTCTGC TTCTTTTCCC  
3360  
ATGCCGGTCA TGCTAACTTT GAAAGCTTCA GCTCTTTCCT TCCTCAATCC TTCTCCTGGC  
3420  
ACCTCTGATA TGCCTTTTGA AATTCATGTT AAAGAATCCC TAGGCTGCTA TCACATGTGG  
3480  
CATCTTTGTT GAGTACATGA ATAAATCAAC TGGTGTGTTT TACGAAGGAT GATTATGCTT  
3540  
CATTGTGGGA TTGTATTTTT CTCTTCTAT CACAGGGAGA AGTGAA  
3586

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TAGGTCAGAT GCAGAAAATT GCCTAAAGAG GAAGGACCAA GGAGATGAAG CAAACACATT  
60  
AAGCCTTCCA CACTCACCTC TAAAACAGTC CTTCAAACCTT CCAGTGCAAC ACTGAAGCTC  
120  
TTGAAGACAC TGAAATATAC ACACAGCAGT AGCAGTAGAT GCATGTACCC TAAGGTCATT  
180  
ACCACAGGCC AGGGGCTGGG CAGCGTACTC ATCATCAACC CTAAAAAGCA GAGCTTTGCT  
240  
TCTCTCTCTA AAATGAGTTA CCTACATTTT AATGCACCTG AATGTTAGAT AGTTACTATA  
300  
TGCCGCTACA AAAAGGTAAA ACTTTTTATA TTTTATACAT TAACTTCAGC CAGCTATTGA  
360  
TATAAATAAA ACATTTTCAC ACAATACAAT AAGTTAACTA TTTTATTTTC TAATGTGCCT  
420  
AGTTCTTTCC CTGCTTAATG AAAAGCTT  
448

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